**RAW SEQUENCE LISTING**
**PATENT APPLICATION:  US/10/004,502**

DATE: 12/12/2001
TIME: 14:28:17

Input Set : A:\BB1470 US NA Seq listing.txt
Output Set: N:\CRF3\12112001\I004502.raw

**ENTERED**

```
     2 <110> APPLICANT: Harvell, Leslie T.
     3        Ragghianti, James J
W--> 5 <110> APPLICANT:
     7 <130> FILE REFERENCE: BB1470 US NA
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/004,502
C--> 10 <141> CURRENT FILING DATE: 2001-10-30
    12 <150> PRIOR APPLICATION NUMBER: 60/244,272
    13 <151> PRIOR FILING DATE: 2000-10-30
    15 <160> NUMBER OF SEQ ID NOS: 13
    17 <170> SOFTWARE: Microsoft Office 97
    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 1493
    21 <212> TYPE: DNA
    22 <213> ORGANISM: Zea mays
    24 <400> SEQUENCE: 1
    25 gcacgagaca atcgcctcgc cttcccttcc ccaccagccc gtctctctct tctctctgtc   60
    26 tctcttctcg taaccgcgtc cacctcgcag cagcaagcaa gcgcgaccaa atggcgcctc  120
    27 taggagacgg cggagctgct gccgcggcgg cgtccaacaa cctggtggtg tcgttcggcg  180
    28 agatgctgat cgacttcgtc cccgacgtgg ccgggctgtc gctggccgag tcgggcggct  240
    29 tcgtcaaggc ccccggcggc gcgcccgcca acgtcgcctg cgccatcgcc aagctcggcg  300
    30 gatcctccgc cttcgtcggc aagttcggcg acgacgagtt cgggcacatg ttggtgaaca  360
    31 tcctgaagca gaacaacgtg aactcggagg ggtgcctgtt cgacaagcac gcgcggacgg  420
    32 cgctggcctt cgtgacgctc aagcacgacg gggagcgcga gttcatgttc tacaggaacc  480
    33 cgagcgcgga catgctgctg acggaggcgg agctggacct gggcctggtg cggcgcgcca  540
    34 aggtgttcca ctacggctcc atctcgctca tctccgagcc gtgccgctcg gcgcacatgg  600
    35 ccgccatgcg cgcagccaag gccgcgggcg tgctctgctc ctacgacccc aacgtgcgcc  660
    36 tcccgctctg gccgtcgccc gacgccgcac gcgagggcat cctcagcatc tggaaggagg  720
    37 ccgacttcat caaggtcagc gacgacgagg tggccttcct cacgcgcggg gacgccaacg  780
    38 acgagaagaa cgtgctgtcc ctgtggtttg acgggctcaa gctgctcgtc gtcaccgacg  840
    39 gggacaaggg atgcaggtac ttcaccaagg acttcaaggg cagcgtgccc ggcttcaagg  900
    40 tcgacaccgt cgacaccacc ggcgccggcg acgccttcgt cggctccctc ctcgtcaacg  960
    41 tcgccaagga cgactccatc ttccacaacg aggagaagct ccgcgaggct ctcaagttct 1020
    42 ccaacgcctg cggcgccatc tgcaccacca agaagggcgc catcccggcg ctgcccacgg 1080
    43 tcgccaccgc ccaggacctc atcgccaagg ccaactagat ggccgcacgc cccgccgttc 1140
    44 caccacgtca ctgtcccccg ccgccccgcc cctcgtcgtc gacgtcctcg gtttcggttc 1200
    45 attaggtaga tcgagtctta gcgtccgtct ctgcgcctct acgctgagac ggtttgtttg 1260
    46 ggttaattaa gttagctttc gtggagattt cgccccgggg catcaataaa atgttggcat 1320
    47 gcgtggtggg atgctatcct ttttttttat tttattttat tttattttta gcttggatca 1380
    48 gttggggttt tgaacattgc tagtgtcgtg tgattgggaa ggctaatgtg atgccttcga 1440
    49 tgcagagttt tcaatgaatg ccttggtgca aacgtaaaaa aaaaaaaaa aaa          1493
    52 <210> SEQ ID NO: 2
    53 <211> LENGTH: 371
    54 <212> TYPE: PRT
    55 <213> ORGANISM: Zea mays
    57 <400> SEQUENCE: 2
    58 Thr Arg Gln Ser Pro Arg Leu Pro Phe Pro Thr Ser Pro Ser Leu Ser
    59  1               5                  10                  15
```

RAW SEQUENCE LISTING                    DATE: 12/12/2001
PATENT APPLICATION:  US/10/004,502      TIME: 14:28:17

Input Set : A:\BB1470 US NA Seq listing.txt
Output Set: N:\CRF3\12112001\I004502.raw

```
61 Ser Leu Cys Leu Ser Ser Arg Asn Arg Val His Leu Ala Ala Ala Ser
62         20              25              30
64 Lys Arg Asp Gln Met Ala Pro Leu Gly Asp Gly Gly Ala Ala Ala Ala
65         35              40              45
67 Ala Ala Ser Asn Asn Leu Val Val Ser Phe Gly Glu Met Leu Ile Asp
68     50              55              60
70 Phe Val Pro Asp Val Ala Gly Leu Ser Leu Ala Glu Ser Gly Gly Phe
71 65              70              75              80
73 Val Lys Ala Pro Gly Gly Ala Pro Ala Asn Val Ala Cys Ala Ile Ala
74             85              90              95
76 Lys Leu Gly Gly Ser Ser Ala Phe Val Gly Lys Phe Gly Asp Asp Glu
77         100             105             110
79 Phe Gly His Met Leu Val Asn Ile Leu Lys Gln Asn Asn Val Asn Ser
80         115             120             125
82 Glu Gly Cys Leu Phe Asp Lys His Ala Arg Thr Ala Leu Ala Phe Val
83     130             135             140
85 Thr Leu Lys His Asp Gly Glu Arg Glu Phe Met Phe Tyr Arg Asn Pro
86 145             150             155             160
88 Ser Ala Asp Met Leu Leu Thr Glu Ala Glu Leu Asp Leu Gly Leu Val
89             165             170             175
91 Arg Arg Ala Lys Val Phe His Tyr Gly Ser Ile Ser Leu Ile Ser Glu
92         180             185             190
94 Pro Cys Arg Ser Ala His Met Ala Ala Met Arg Ala Ala Lys Ala Ala
95         195             200             205
97 Gly Val Leu Cys Ser Tyr Asp.Pro Asn Val Arg Leu Pro Leu Trp Pro
98     210             215             220
100 Ser Pro Asp Ala Ala Arg Glu Gly Ile Leu Ser Ile Trp Lys Glu Ala
101 225             230             235             240
103 Asp Phe Ile Lys Val Ser Asp Asp Glu Val Ala Phe Leu Thr Arg Gly
104             245             250             255
106 Asp Ala Asn Asp Glu Lys Asn Val Leu Ser Leu Trp Phe Asp Gly Leu
107         260             265             270
109 Lys Leu Leu Val Val Thr Asp Gly Asp Lys Gly Cys Arg Tyr Phe Thr
110         275             280             285
112 Lys Asp Phe Lys Gly Ser Val Pro Gly Phe Lys Val Asp Thr Val Asp
113     290             295             300
115 Thr Thr Gly Ala Gly Asp Ala Phe Val Gly Ser Leu Leu Val Asn Val
116 305             310             315             320
118 Ala Lys Asp Asp Ser Ile Phe His Asn Glu Glu Lys Leu Arg Glu Ala
119             325             330             335
121 Leu Lys Phe Ser Asn Ala Cys Gly Ala Ile Cys Thr Thr Lys Lys Gly
122         340             345             350
124 Ala Ile Pro Ala Leu Pro Thr Val Ala Thr Ala Gln Asp Leu Ile Ala
125         355             360             365
127 Lys Ala Asn
128     370
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 430
133 <212> TYPE: DNA
```

RAW SEQUENCE LISTING                    DATE: 12/12/2001
PATENT APPLICATION:  US/10/004,502      TIME: 14:28:17

Input Set : A:\BB1470 US NA Seq listing.txt
Output Set: N:\CRF3\12112001\I004502.raw

```
    134 <213> ORGANISM: Zea mays
    136 <220> FEATURE:
    137 <221> NAME/KEY: unsure
    138 <222> LOCATION: (293)
    139 <223> OTHER INFORMATION: n = A, C, G or T
    141 <400> SEQUENCE: 3
    142 gcgacgacga gttcggccgc atgctcgccg ccatcctccg cgacaacggc gtcgacggcg  60
    143 gcggcgtcgt cttcgacgcg ggcgcgcgca ccgccttgcc ttcgtcaccc tgcgcgccga 120
    144 cggcgagcgc gagttcatgt tctaccgcaa ccccagcgcc gacatgctcc tcactgccga 180
    145 cgagctcaac gtcgggctca tccggagggc tgcggtcttt cactacggat caataagctt 240
W--> 146 gattgctgag ccttgccgga cagcacatct ccgtgccatg gaaattgcca aanaggctgg 300
    147 tgcactgctc tcttacgacc caaacctgag ggaggcactt tggccatccc gtgaggaggc 360
    148 ccgcacccag atcttgagca ttgggaccag gcagatatcg tcaaggtcag cgaagtcgag 420
    149 cttgagtttt                                                        430
    152 <210> SEQ ID NO: 4
    153 <211> LENGTH: 101
    154 <212> TYPE: PRT
    155 <213> ORGANISM: Zea mays
    157 <220> FEATURE:
    158 <221> NAME/KEY: UNSURE
    159 <222> LOCATION: (72)
    160 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
    162 <400> SEQUENCE: 4
    163 Gly Arg Ala His Arg Leu Ala Phe Val Thr Leu Arg Ala Asp Gly Glu
    164  1               5                  10                  15
    166 Arg Glu Phe Met Phe Tyr Arg Asn Pro Ser Ala Asp Met Leu Leu Thr
    167             20                  25                  30
    169 Ala Asp Glu Leu Asn Val Gly Leu Ile Arg Arg Ala Ala Val Phe His
    170             35                  40                  45
    172 Tyr Gly Ser Ile Ser Leu Ile Ala Glu Pro Cys Arg Thr Ala His Leu
    173         50                  55                  60
W--> 175 Arg Ala Met Glu Ile Ala Lys Xaa Ala Gly Ala Leu Leu Ser Tyr Asp
    176  65                  70                  75                  80
    178 Pro Asn Leu Arg Glu Ala Leu Trp Pro Ser Arg Glu Glu Ala Arg Thr
    179                 85                  90                  95
    181 Gln Ile Leu Ser Ile
    182             100
    185 <210> SEQ ID NO: 5
    186 <211> LENGTH: 1553
    187 <212> TYPE: DNA
    188 <213> ORGANISM: Oryza sativa
    190 <400> SEQUENCE: 5
    191 gcacgagctt acactcatct catctcatct caccctcgcc gcgcgccgag gaagacgcgc  60
    192 atctcctctc tccctctata taagcgcgcg cctcgccacc tcacccgaag aaattcccca 120
    193 ccattccatc tctctctctc tcgaatcttg atctctctct ttcatcgcct cttgtgttcg 180
    194 cgcgcgcgag cagggtggtt gttgttggtg ggggtgcaat ggcggggagg agcgagctgg 240
    195 tggtgagctt cggggagatg ctgatagact tcgtgccgac ggtggcgggg gtgtcgctgg 300
    196 cggaggcgcc ggcgttcgtc aaggcgccag ggggggcgcc ggcgaacgtg gccatcgcgg 360
    197 tggcgcggct cggcggcggg gccgcgttcg tcggcaagct gggggacgac gagttcgggc 420
```

RAW SEQUENCE LISTING         DATE: 12/12/2001
PATENT APPLICATION:  US/10/004,502    TIME: 14:28:17

Input Set : A:\BB1470 US NA Seq listing.txt
Output Set: N:\CRF3\12112001\I004502.raw

```
198 ggatgctcgc ggccatcctc cgcgacaacg gcgtcgacga cggcggggtc gtgttcgacg  480
199 ccggggcgcg caccgcgctc gccttcgtca ccctccgcgc cgacggggag cgcgagttca  540
200 tgttctaccg caaccccagc gccgacatgc tcctcaccca cgccgagctc aacgtcgagc  600
201 tcatcaagag ggctgccgtc ttccattatg gatcaataag cttgatagct gagccctgcc  660
202 ggtcagcaca tttgcgtgcc atggagattg cgaaagaagc tggtgcgctg ctatcttatg  720
203 acccgaatct cagggaggca ttgtggccct cccgtgagga ggctcgcacc aagatcttga  780
204 gcatctggga ccaggcagac attgtcaagg tcagcgaggt cgagcttgag ttcttgaccg  840
205 gcattgactc agtagaggat gatgttgtca tgaagctatg gcgccctacc atgaagctcc  900
206 tccttgtgac tcttggagat caaggatgca agtactatgc cagggatttc cgcggagctg  960
207 tcccatccta caaagtacag caagttgata caacaggtgc aggtgatgcg tttgttggtg 1020
208 ctctgctgcg aagaattgtc caggatccat catcgttgca agatcagaag aagcttgagg 1080
209 aagcgattaa atttgccaat gcgtgcggag caatcaccgc cacaaagaaa ggggcaatcc 1140
210 catcactgcc caccgaagtt gaggtcttga agttgatgga gagtgcttag atcgatcagt 1200
211 agcattatgg tcactagctt cagcttccgc aaattgtatt gtatgctgat ctggatcagg 1260
212 agcagggggg tactccaaga tgcctgcctt tttgttgcca acttcccttc ctggcaggat 1320
213 ttttgatttg gaactctaat ttgaataagc agagccgttc aatgtcagtt tctactatat 1380
214 gattaaataa tcggtcctta attgtaatgc atcattcttt tttttttttt aactgaatcc 1440
215 ttgttccatg ctgtatgaac tcctttgagt tccatttgta tatggtgctc ttgccattat 1500
216 aagagtagtg tttggtccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa         1553
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 368
221 <212> TYPE: PRT
222 <213> ORGANISM: Oryza sativa
224 <400> SEQUENCE: 6
225 Ala Arg Ala Ser Pro Pro His Pro Lys Lys Phe Pro Thr Ile Pro Ser
226  1               5                  10                  15
228 Leu Ser Leu Ser Asn Leu Asp Leu Ser Leu Ser Ser Pro Leu Val Phe
229                 20                  25                  30
231 Ala Arg Ala Ser Arg Val Val Val Val Gly Gly Gly Ala Met Ala Gly
232             35                  40                  45
234 Arg Ser Glu Leu Val Val Ser Phe Gly Glu Met Leu Ile Asp Phe Val
235         50                  55                  60
237 Pro Thr Val Ala Gly Val Ser Leu Ala Glu Ala Pro Ala Phe Val Lys
238  65                  70                  75                  80
240 Ala Pro Gly Gly Ala Pro Ala Asn Val Ala Ile Ala Val Ala Arg Leu
241                 85                  90                  95
243 Gly Gly Gly Ala Ala Phe Val Gly Lys Leu Gly Asp Asp Glu Phe Gly
244             100                 105                 110
246 Arg Met Leu Ala Ala Ile Leu Arg Asp Asn Gly Val Asp Asp Gly Gly
247         115                 120                 125
249 Val Val Phe Asp Ala Gly Ala Arg Thr Ala Leu Ala Phe Val Thr Leu
250     130                 135                 140
252 Arg Ala Asp Gly Glu Arg Glu Phe Met Phe Tyr Arg Asn Pro Ser Ala
253 145                 150                 155                 160
255 Asp Met Leu Leu Thr His Ala Glu Leu Asn Val Glu Leu Ile Lys Arg
256                 165                 170                 175
258 Ala Ala Val Phe His Tyr Gly Ser Ile Ser Leu Ile Ala Glu Pro Cys
259             180                 185                 190
261 Arg Ser Ala His Leu Arg Ala Met Glu Ile Ala Lys Glu Ala Gly Ala
```

```
262         195              200              205
264 Leu Leu Ser Tyr Asp Pro Asn Leu Arg Glu Ala Leu Trp Pro Ser Arg
265     210              215              220
267 Glu Glu Ala Arg Thr Lys Ile Leu Ser Ile Trp Asp Gln Ala Asp Ile
268 225              230              235              240
270 Val Lys Val Ser Glu Val Glu Leu Glu Phe Leu Thr Gly Ile Asp Ser
271             245              250              255
273 Val Glu Asp Asp Val Val Met Lys Leu Trp Arg Pro Thr Met Lys Leu
274             260              265              270
276 Leu Leu Val Thr Leu Gly Asp Gln Gly Cys Lys Tyr Tyr Ala Arg Asp
277     275              280              285
279 Phe Arg Gly Ala Val Pro Ser Tyr Lys Val Gln Gln Val Asp Thr Thr
280     290              295              300
282 Gly Ala Gly Asp Ala Phe Val Gly Ala Leu Leu Arg Arg Ile Val Gln
283 305              310              315              320
285 Asp Pro Ser Ser Leu Gln Asp Gln Lys Lys Leu Glu Glu Ala Ile Lys
286             325              330              335
288 Phe Ala Asn Ala Cys Gly Ala Ile Thr Ala Thr Lys Lys Gly Ala Ile
289             340              345              350
291 Pro Ser Leu Pro Thr Glu Val Glu Val Leu Lys Leu Met Glu Ser Ala
292     355              360              365
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 1310
297 <212> TYPE: DNA
298 <213> ORGANISM: Glycine max
300 <400> SEQUENCE: 7
301 gcacgagaga actagtctct cgtgccgctc gaaaacagtg ttccaaaatc caaacacact   60
302 ctctctcccc atggcgttga acaatggcgt ccccgccacc ggcaccggcc tcatcgtcag  120
303 cttcggtgag atgctcatcg acttcgtccc caccgtctct ggcgtgtccc tggccgaggc  180
304 ccctggcttc ctcaaggccc ccggcggcgc ccccgctaac gtcgccatcg ccgtgtcgcg  240
305 cctcggcggc aaagccgcct tcgtcggcaa gctcggcgac gacgagttcg gccacatgct  300
306 cgccggaatc ctcaaggaaa acggcgttcg cgccgacggc atcaactttg accagggcgc  360
307 acgcaccgcc ctggccttcg tgaccctacg cgccgacggg gagcgtgagt tcatgttcta  420
308 cagaaacccc agcgccgaca tgctcctcaa gcccgaagaa ctcaatctcg aactcatcag  480
309 atctgcaaaa gttttccatt acggatcaat cagtttgatc gtggagccat gcagatcagc  540
310 acacttgaag gcaatggaag tagccaagga atctgggtgc ttgctctcct atgaccccaa  600
311 ccttcgtcta cctttgtggc cttcggctga ggaagctcgt aagcaaatac tgagcatttg  660
312 ggagaaggct gatttgatca aggtcagtga tgcggagctt gagttcctca caggaagtga  720
313 caagattgat gatgaatctg ctttgtcatt gtggcacccc aatttgaagt tgctccttgt  780
314 cactcttggg gaacatggtt ccagatacta caccaagagt ttcaaaggat cggtagatgc  840
315 tttccatgtc aatacagttg atacaactgg tgccggtgat tcctttgttg gtgctttatt  900
316 ggccaagatt gtcgatgatc agtccatact tgaagatgaa ccaaggttaa gagaagtact  960
317 aaagtttgca aatgcatgtg gagctattac aactacccaa aagggagcaa ttccggccct 1020
318 tcccaaagag gaggctgcac tgaaactgat caaaggggggg tcatagaatc ttttggcaaa 1080
319 atgcaaaagt gctagcatga tttcgttttc ttcccctaat gtttaaattt tccgttggat 1140
320 ttgcttgcta taagtttagg agggaacttt tgttttttct cctatgcact gttttcaggt 1200
321 tttgccaaat aacgctttct ttcaaatttt gagattagcg attgaatgaa aatttgaatc 1260
322 ataagctcgg cccatagttg caacttaaaa aaaaaaaaa aaaaaaaaa       1310
325 <210> SEQ ID NO: 8
```

**VERIFICATION SUMMARY**                 DATE: 12/12/2001
PATENT APPLICATION:  US/10/004,502       TIME: 14:28:18

Input Set : **A:\BB1470 US NA Seq listing.txt**
Output Set: **N:\CRF3\12112001\I004502.raw**

```
L:5 M:201 W: Mandatory field data missing, TITLE INVENTION
L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
```